Mouse Sox9 Sequence

```
   1  AGTTTCAGTC CAGGAACTTT TCTTTGCAAG AGAGACGAGG TGCAAGTGGC
  51  CCCGGTTTCG TTCTCTGTTT TCCCTCCCTC CTCCTCCGCT CCGACTCGCC
 101  TTCCCCGGGT TTAGAGCCGG CAGCTGAGAC CCGCCACCCA GCGCCTCTGC
 151  TAAGTGCCCG CCGCCGCAGC CCGGTGACGC GCCAACCTCC CCGGGAGCCG
 201  TTCGCTCGGC GTCCGCGTCC GGGCAGCTGA GGGAAGAGGA GCCCCAGCCG
 251  CCGCGGCTTC TCGCCTTTCC CGGCCACCCG CCCCCTGCCC CGGGCTCGCG
 301  TATGAATCTC CTGGACCCCT TCATGAAGAT GACCGACGAG CAGGAGAAGG
 351  GCCTGTCTGG CGCCCCCAGC CCCACCATGT CGGAGGACTC GGCTGGTTCG
 401  CCCTGTCCCT CGGGCTCCGG CTCGGACACG GAGAACACCC GGCCCCAGGA
 451  GAACACCTTC CCCAAGGGCG AGCCGGATCT GAAGAAGGAG AGCGAGGAAG
 501  ATAAGTTCCC CGTGTGCATC CGCGAGGCGG TCAGCCAGGT GCTGAAGGGC
 551  TACGACTGGA CGCTGGTGCC CATGCCCGTG CGCGTCAACG GCTCCAGCAA
 601  GAACAAGCCA CACGTCAAGC GACCCATGAA CGCCTTCATG GTGTGGGCGC
 651  AGGCTGCGCG CAGGAAGCTG GCAGACCAGT ACCCGCATCT GCACAACGCG
 701  GAGCTCAGCA AGACTCTGGG CAAGCTCTGG AGGCTGCTGA ACGAGAGCGA
 751  GAAGAGACCC TTCGTGGAGG AGGCGGAGCG GCTGCGCGTG CAGCACAAGA
 801  AAGACCACCC CGATTACAAG TACCAGCCCC GGCGGAGGAA GTCGGTGAAG
 851  AACGGACAAG CGGAGGCCGA AGAGGCCACG GAACAGACTC ACATCTCTCC
 901  TAATGCTATC TTCAAGGCGC TGCAAGCCGA CTCCCCACAT TCCTCCTCCG
 951  GCATGAGTGA GGTGCACTCC CCGGGCGAGC ACTCTGGGCA ATCTCAGGGT
1001  CCGCCGACCC CACCCACCAC TCCCAAAACC GACGTGCAAG CTGGCAAAGT
1051  TGATCTGAAG CGAGAGGGGC GCCCTCTGGC AGAGGGGGGC AGACAGCCCC
1101  CCATCGACTT CCGCGACGTG GACATCGGTG AACTGAGCAG CGACGTCATC
1151  TCCAACATTG AGACCTTCGA CGTCAATGAG TTTGACCAAT ACTTGCCACC
1201  CAACGGCCAC CCAGGGGTTC CGGCCACCCA CGGCCAGGTC ACCTACACTG
1251  GCAGTTACGG CATCAGCAGC ACCGCACCCA CCCCTGCGAC CGCGGGCCAC
```

Figure 1(a)

1301 GTGTGGATGT CGAAGCAGCA GGCGCCGCCC CCTCCTCCGC AGCAGCCTCC

1351 GCAGGCCCCG CAAGCCCCAC AGGCGCCTCC GCAGCAGCAA GCACCCCCGC

1401 AGCAGCCGCA GGCACCCCAG CAGCAGCAGG CACACACGCT CACCACGCTG

1451 AGCAGCGAGC CAGGCCAGTC CCAGCGAACG CACATCAAGA CGGAGCAGCT

1501 GAGCCCCAGC CACTACAGGG AGCAGCAGCA GCACTCCCCG CAACAGATCT

1551 CCTACAGCCC CTTCAACCTT CCTCACTACA GGCCCTCCTA CCCGCCCATC

1601 ACCCGTTCGG AATACGACTA CGCTGACCAT CAGAACTCCG GCTCCTACTA

1651 CAGTCACGCA GCCGGCCAGG GCTCAGGGCT CTACTCCACC TTCACTTACA

1701 TGAACCCCGC GCAGCGCCCC ATGTACACCC CCATCGGTGA CACCTCCGGG

1751 GTCCCTTCCA TCCCGCAGAC CCACAGCCCG CAGGACTGGG AACAACCAGT

1801 CTACACACAG GTCACCAGAC CCTGAGAAGA GAAAAGCTAT GGTGACAGAG

1851 CTGATCTTTT TTTTTTTTTT TTTTTAAAGA AGAAAAGAAA GAAACGAAAA

1901 AGAAAAAGCT GAAGGAAATC AAGAACCAAT TGAAATTCCT TTGGACACTT

1951 TTTTTTTTGT CCTTTCGTTA ATTTTTAAAA GACATGTAAA GGAAGGTAAC

2001 GATTGCTGGG CATTCCAGGA GAGAGACTTT AAGACTTTGT CTGAGCTCAT

2051 GACAACATAT TGCAAATGGC CGGGCCACTC GTGGCCAGAC GGACAGCACT

2101 CCTGGCCAGA TGGACCCACC AGTATCAGCG AGGAGGGGCT TGTCTCCTTC

2151 AGAGTTAACA TGGAGGACGA TTGGAGAATC TCCCTGCCTG TTTGGACTTT

2201 GTAATTATTT TTTAGCCGTA ATTAAAGAAA AAAAAAGTCC AAAAAAAAA

Figure 1(b)

Mouse Sox-9 amino acid sequence

```
Met Asn Leu Leu Asp Pro Phe Met Lys Met Thr Asp Glu Gln Glu Lys
1               5                  10                  15

Gly Leu Ser Gly Ala Pro Ser Pro Thr Met Ser Glu Asp Ser Ala Gly
            20                  25                  30

Ser Pro Cys Pro Ser Gly Ser Gly Ser Asp Thr Glu Asn Thr Arg Pro
        35                  40                  45

Gln Glu Asn Thr Phe Pro Lys Gly Glu Pro Asp Leu Lys Lys Glu Ser
    50                  55                  60

Glu Glu Asp Lys Phe Pro Val Cys Ile Arg Glu Ala Val Ser Gln Val
65                  70                  75                  80

Leu Lys Gly Tyr Asp Trp Thr Leu Val Pro Met Pro Val Arg Val Asn
                85                  90                  95

Gly Ser Ser Lys Asn Lys Pro His Val Lys Arg Pro Met Asn Ala Phe
            100                 105                 110

Met Val Trp Ala Gln Ala Ala Arg Arg Lys Leu Ala Asp Gln Tyr Pro
        115                 120                 125

His Leu His Asn Ala Glu Leu Ser Lys Thr Leu Gly Lys Leu Trp Arg
    130                 135                 140

Leu Leu Asn Glu Ser Glu Lys Arg Pro Phe Val Glu Glu Ala Glu Arg
145                 150                 155                 160

Leu Arg Val Gln His Lys Lys Asp His Pro Asp Tyr Lys Tyr Gln Pro
                165                 170                 175

Arg Arg Arg Lys Ser Val Lys Asn Gly Gln Ala Glu Ala Glu Glu Ala
            180                 185                 190

Thr Glu Gln Thr His Ile Ser Pro Asn Ala Ile Phe Lys Ala Leu Gln
        195                 200                 205

Ala Asp Ser Pro His Ser Ser Ser Gly Met Ser Glu Val His Ser Pro
    210                 215                 220

Gly Glu His Ser Gly Gln Ser Gln Gly Pro Pro Thr Pro Pro Thr Thr
225                 230                 235                 240

Pro Lys Thr Asp Val Gln Ala Gly Lys Val Asp Leu Lys Arg Glu Gly
                245                 250                 255

Arg Pro Leu Ala Glu Gly Gly Arg Gln Pro Pro Ile Asp Phe Arg Asp
            260                 265                 270
```

Figure 1(c)

```
Val Asp Ile Gly Glu Leu Ser Ser Asp Val Ile Ser Asn Ile Glu Thr
        275                 280                 285

Phe Asp Val Asn Glu Phe Asp Gln Tyr Leu Pro Pro Asn Gly His Pro
    290                 295                 300

Gly Val Pro Ala Thr His Gly Gln Val Thr Tyr Thr Gly Ser Tyr Gly
305                 310                 315                 320

Ile Ser Ser Thr Ala Pro Thr Pro Ala Thr Ala Gly His Val Trp Met
                325                 330                 335

Ser Lys Gln Gln Ala Pro Pro Pro Pro Pro Gln Gln Pro Pro Gln Ala
            340                 345                 350

Pro Gln Ala Pro Gln Ala Pro Pro Gln Gln Gln Ala Pro Pro Gln Gln
        355                 360                 365

Pro Gln Ala Pro Gln Gln Gln Gln Ala His Thr Leu Thr Thr Leu Ser
    370                 375                 380

Ser Glu Pro Gly Gln Ser Gln Arg Thr His Ile Lys Thr Glu Gln Leu
385                 390                 395                 400

Ser Pro Ser His Tyr Arg Glu Gln Gln Gln His Ser Pro Gln Gln Ile
                405                 410                 415

Ser Tyr Ser Pro Phe Asn Leu Pro His Tyr Arg Pro Ser Tyr Pro Pro
            420                 425                 430

Ile Thr Arg Ser Glu Tyr Asp Tyr Ala Asp His Gln Asn Ser Gly Ser
        435                 440                 445

Tyr Tyr Ser His Ala Ala Gly Gln Gly Ser Gly Leu Tyr Ser Thr Phe
    450                 455                 460

Thr Tyr Met Asn Pro Ala Gln Arg Pro Met Tyr Thr Pro Ile Gly Asp
465                 470                 475                 480

Thr Ser Gly Val Pro Ser Ile Pro Gln Thr His Ser Pro Gln Asp Trp
                485                 490                 495

Glu Gln Pro Val Tyr Thr Gln Val Thr Arg Pro
            500                 505
```

Figure 1(d)

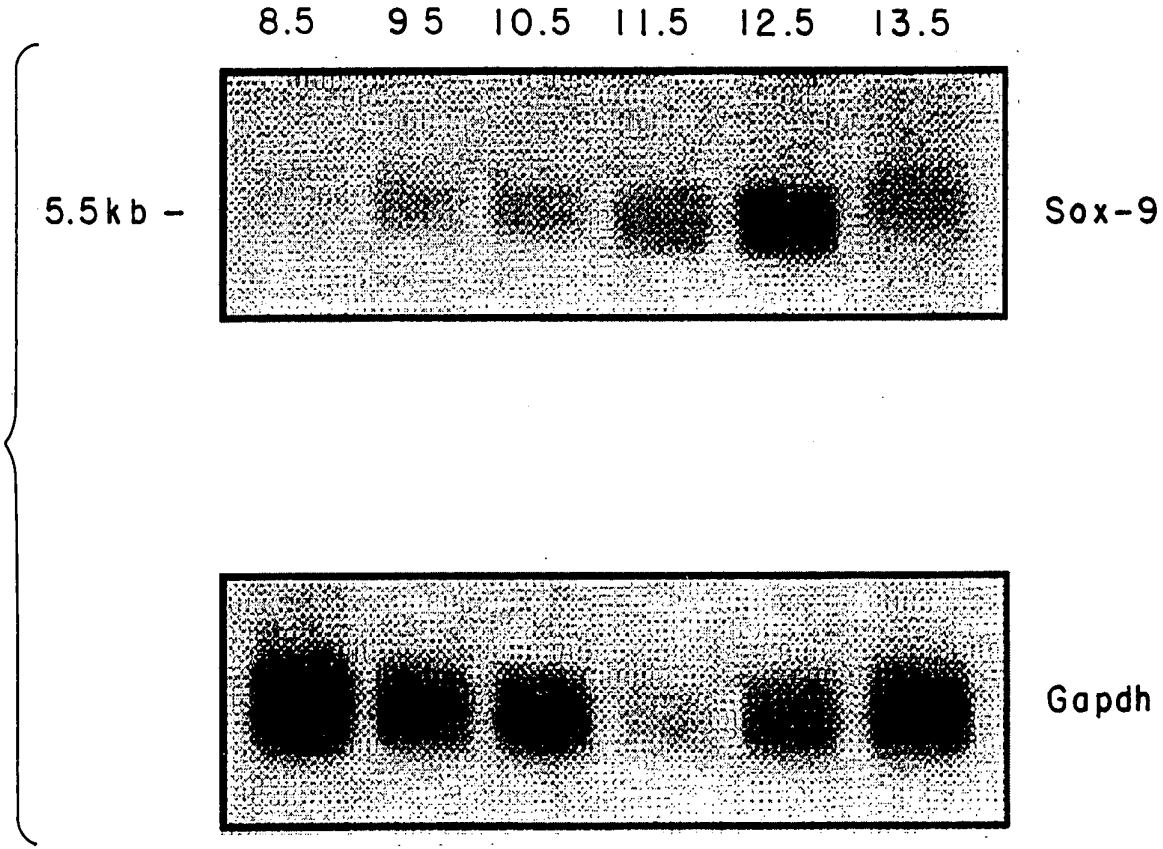

FIG.2

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

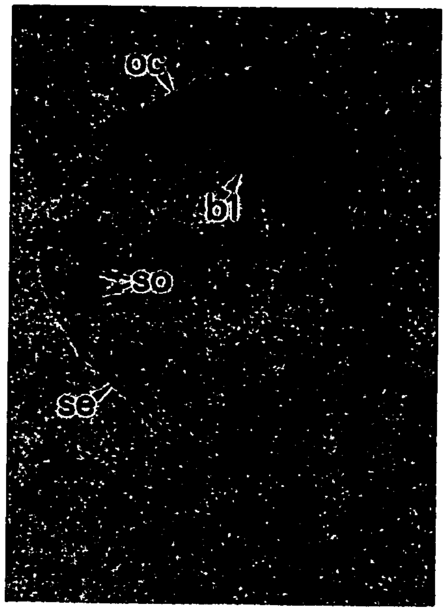

FIG.3a

FIG.3b

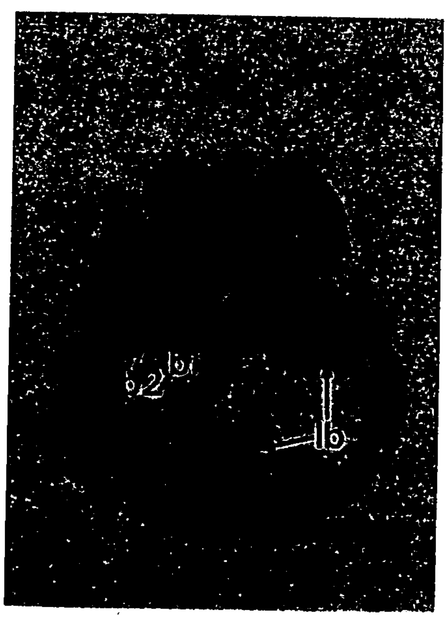

FIG.3c

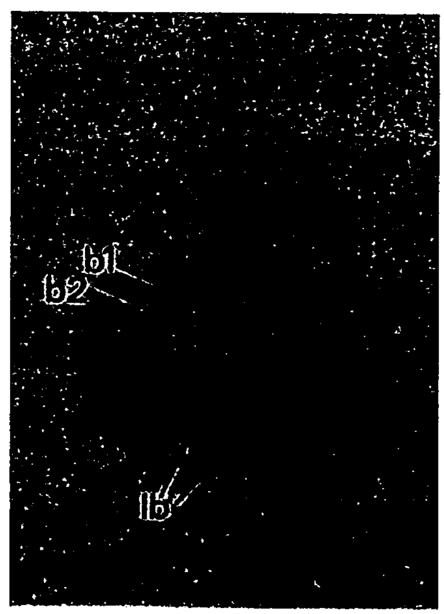

FIG.3d

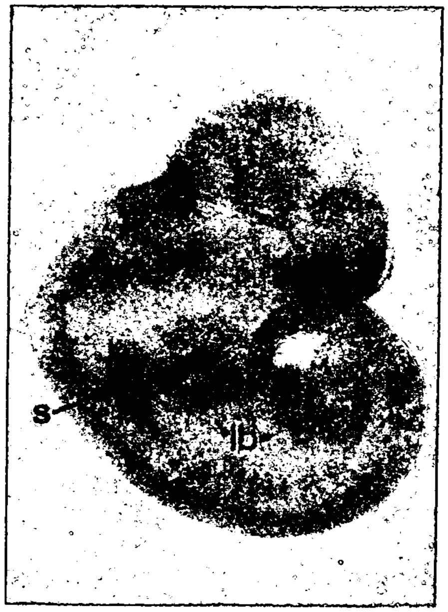

FIG.3e

FIG.3f

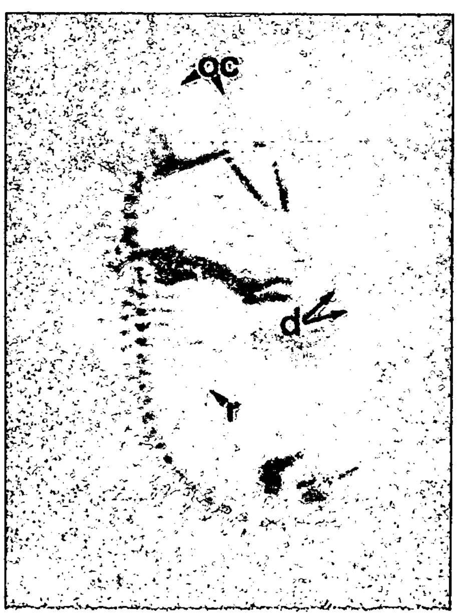

FIG.3g

FIG.3h

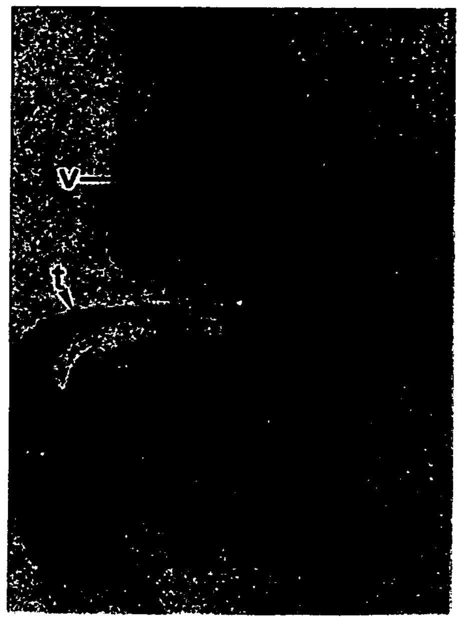

FIG.3i

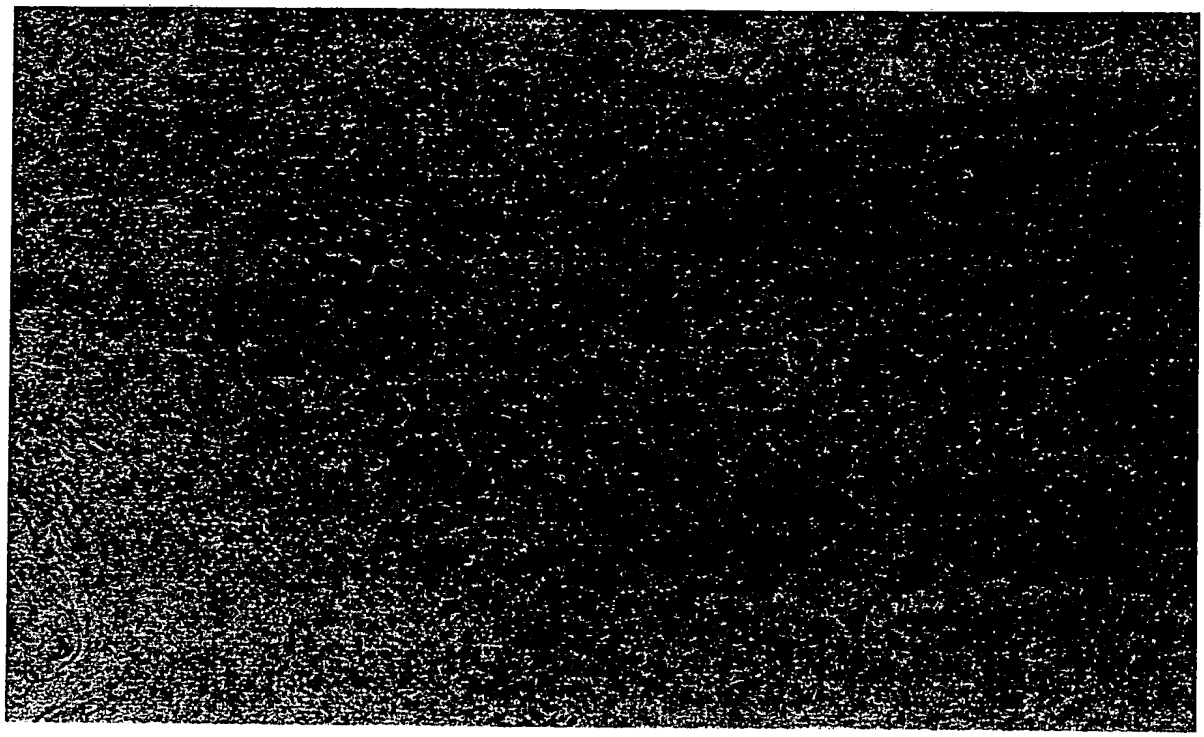

FIG.4

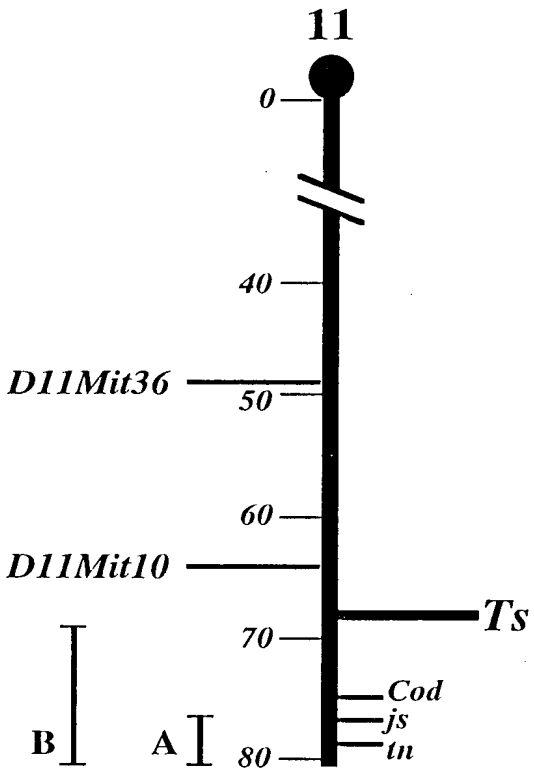

FIG.5

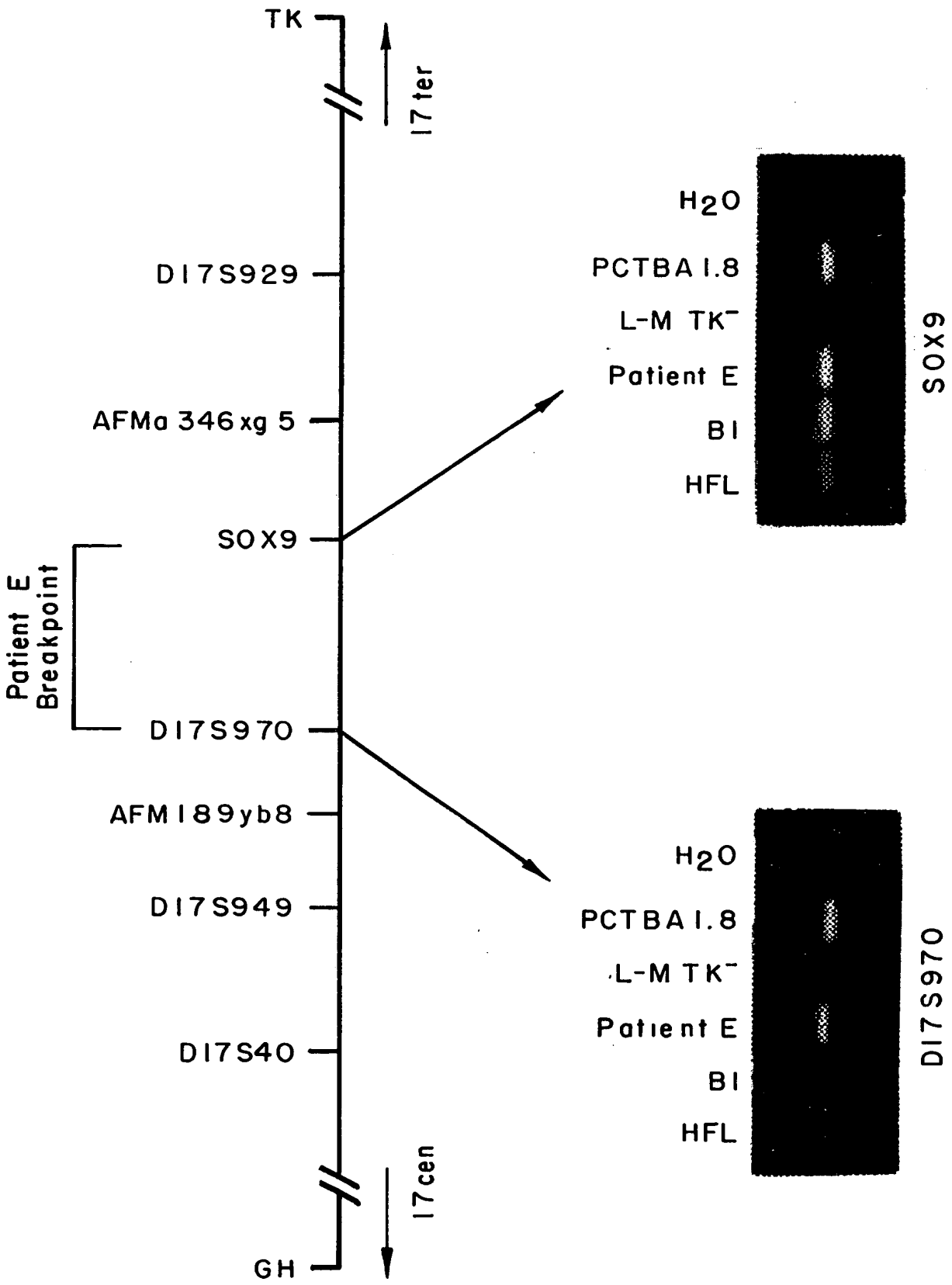

FIG.6

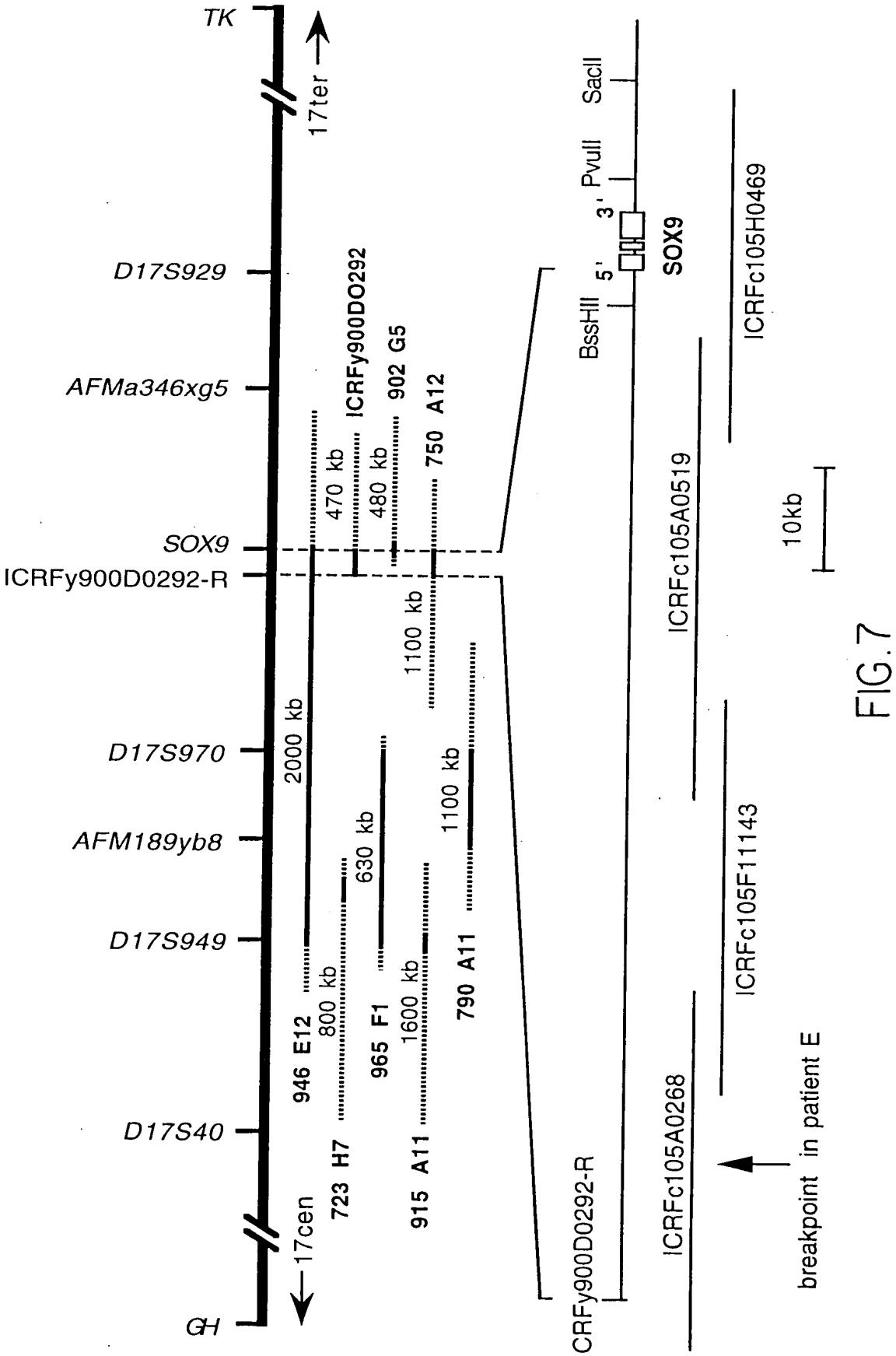

FIG. 7

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

CGGAGCTCGA AACTGACTGG AAACTTCAGT GGCGCGGAGA CTCGCCAGTT TCAACCCCGG
AAACTTTTCT TTGCAGGAGG AGAAGAGAAG GGGTGCAAGC GCCCCCACTT TTGCTCTTTT
TCCTCCCCTC CTCCTCCTCT CCAATTCGCC TCCCCCCACT TGGAGCGGGC AGCTGTGAAC
TGGCCACCCC GCGCCTTCCT AAGTGCTCGC CGCGGTAGCC GGCCGACGCG CCAGCTTCCC
CGGGAGCCGC TTGCTCCGCA TCCGGGCAGC CGAGGGGAGA GGAGCCCGCG CCTCGAGTCC
CCGAGCCGCC GCGGCTTCTC GCCTTTCCCG GCCACCAGCC CCCTGCCCCG GGCCCGCGTA
TGAATCTCCT GGACCCCTTC ATGAAGATGA CCGACGAGCA GGAGAAGGGC CTGTCCGGCG
CCCCCAGCCC CACCATGTCC GAGGACTCCG CGGGCTCGCC CTGCCCGTCG GGCTCCGGCT
CGGACACCGA GAACACGCGG CCCCAGGAGA ACACGTTCCC CAAGGGCGAG CCCGATCTGA
AGAAGGAGAG CGAGGAGGAC AAGTTCCCCG TGTGCATCCG CGAGGCGGTC AGCCAGGTGC
TCAAAGGCTA CGACTGGACG CTGGTGCCCA TGCCGGTGCG CGTCAACGGC TCCAGCAAGA
ACAAGCCGCA CGTCAAGCGG CCCATGAACG CCTTCATGGT GTGGGCGCAG GCGGCGCGCA
GGAAGCTCGC GGACCAGTAC CCGCACTTGC ACAACGCCGA GCTCAGCAAG ACGCTGGGCA
AGCTCTGGAG ACTTCTGAAC GAGAGCGAGA AGCGGCCCTT CGTGGAGGAG GCGGAGCGGC
TGCGCGTGCA GCACAAGAAG GACCACCCGG ATTACAAGTA CCAGCCGCGG CGGAGGAAGT
CGGTGAAGAA CGGGCAGGCG GAGGCAGAGG AGGCCACGGA GCAGACGCAC ATCTCCCCCA
ACGCCATCTT CAAGGCGCTG CAGGCCGACT CGCCACACTC CTCCTCCGGC ATGAGCGAGG
TGCACTCCCC CGGCGAGCAC TCGGGGCAAT CCCAGGGCCC ACCGACCCCA CCCACCACCC
CCAAAACCGA CGTGCAGCCG GGCAAGGCTG ACCTGAAGCG AGAGGGGCGC CCCTTGCCAG
AGGGGGGCAG ACAGCCCCCT ATCGACTTCC GCGACGTGGA CATCGGCGAG CTGAGCAGCG
ACGTCATCTC CAACATCGAG ACCTTCGATG TCAACGAGTT TGACCAGTAC CTGCCGCCCA
ACGGCCACCC GGGGGTGCCG GCCACGCACG GCCAGGTCAC CTACACGGGC AGCTACGGCA
TCAGCAGCAC CGCGGCCACC CCGGCGAGCG CGGGCCACGT GTGGATGTCC AAGCAGCAGG
CGCCGCCGCC ACCCCCGCAG CAGCCCCCAC AGGCCCCGCC GGCCCCGCAG GCGCCCCCGC
AGCCGCAGGC GGCGCCCCCA CAGCAGCCGG CGGCACCCCC GCAGCAGCCA CAGGCGCACA
CGCTGACCAC GCTGAGCAGC GAGCCGGGCC AGTCCCAGCG AACGCACATC AAGACGGAGC
AGCTGAGCCC CAGCCACTAC AGCGAGCAGC AGCAGCACTC GCCCCAACAG ATCGCCTACA
GCCCCTTCAA CCTCCCACAC TACAGCCCCT CCTACCCGCC CATCACCCGC TCACAGTACG
ACTACACCGA CCACCAGAAC TCCAGCTCCT ACTACAGCCA CGCGGCAGGC CAGGGCACCG
GCCTCTACTC CACCTTCACC TACATGAACC CCGCTCAGCG CCCCATGTAC ACCCCCATCG
CCGACACCTC TGGGGTCCCT TCCATCCCGC AGACCCACAG CCCCCAGCAC TGGGAACAAC
CCGTCTACAC ACAGCTCACT CGACCTTGAG GAGGCCTCCC ACGAAGGGCG ACGATGGCCG
AGATGATCCT AAAAATAACC GAAGAAAGAG AGGACCAACC AGAATTCCCT TTGGACATTT
GTGTTTTTTT GTTTTTTTAT TTTGTTTTGT TTTTTCTTCT TCTTCTTCTT CCTTAAAGAC
ATTTAAGCTA AAGGCAACTC GTACCCAAAT TTCCAAGACA CAAACATGAC CTATCCAAGC
GCATTACCCA CTTGTGGCCA ATCAGTGGCC AGGCCAACCT TGGCTAAATG GAGCAGCGAA
ATCAACGAGA AACTGGACTT TTTAAACCCT CTTCAGAGCA AGCGTGGAGG ATGATGGAGA
ATCGTGTGAT CAGTGTGCTA AATCTCTCTG CCTGTTTGGA CTTTGTAATT ATTTTTTTAG
CAGTAATTAA AGAAAAAAGT CCTCTGTGAG GAATATTCTC TATTTTAAAT ATTTTTAGTA
TGTACTGTGT ATGATTCATT ACCATTTTGA GGGGATTTAT ACATATTTTT AGATAAAATT
AAATGCTCTT ATTTTTCCAA CAGCTAAACT ACTCTTAGTT GAACAGTGTG CCCTAGCTTT
TCTTGCAACC AGAGTATTTT TGTACAGATT TGCTTTCTCT TACAAAAAGA AAAAAAAAAT
CCTGTTGTAT TAACATTTAA AAACAGAATT GTGTTATGTG ATCAGTTTTG GGGGTTAACT
TTGCTTAATT CCTCAGGCTT TGCGATTTAA GGAGGAGCTG CCTTAAAAAA AAATAAAGGC
CTTATTTTGC AATTATGGGA GTAAACAATA GTCTAGAGAA GCATTTGGTA AGCTTTATGA
TATATATATT TTTTAAAGAA GAGAAAAACA CCTTGAGCCT TAAAACGGTG CTGCTGGGAA
ACATTTGCAC TCTTTTAGTG CATTTCCTCC TGCCTTTGCT TGTTCACTGC AGTCTTAAGA
AAGAGGTAAA AGGCAAGCAA AGGAGATGAA ATCTGTTCTG GGAATGTTTC AGCAGCCAAT
AAGTGCCCGA GCACACTGCC CCCGGTTGCC TGCCTGGGCC CCATGTGGAA GGCAGATGCC
TGCTCGCTCT GTCACCTGTG CCTCTCAGAA CACCAGCAGT TAACCTTCAA GACATTCCAC

Figure 8a(1)

```
TTGCTAAAAT TATTTATTTT GTAAGGAGAG GTTTTAATTA AAACAAAAAA AAATTCTTTT
TTTTTTTTTT TTTTCCAATT TTACCTTCTT TAAAATAGGT TGTTGGAGCT TTCCTCAAAG
GGTATGGTCA TCTGTTGTTA AATTATGTTC TTAACTGTAA CCAGTTTTTT TTTATTTATC
TCTTTAATCT TTTTTATTAT TAAAAGCAAG TTTCTTTGTA TTCCTCACCC TAGATTTGTA
TAAATGCCTT TTTGTCCATC CCTTTTTTCT TTGTTGTTTT TGTTGAAAAC AAACTGGAAA
CTTGTTTCTT TTTTTGTATA AATGAGAGAT TGCAAATGTA GTGTATCACT GAGTCATTTG
CAGTGTTTTC TGCCACAGAC CTTTGGGCTG CCTTATATTG TGTGTGTGTG TGGGTGTGTG
TGTGTTTTGA CACAAAAACA ATGCAAGCAT GTGTCATCCA TATTTCTCTA CATCTTCTCT
TGGAGTGAGG GAGGCTACCT GGAGGGGATC AGCCCACTGA CAGACCTTAA TCTTAATTAC
TGCTGTGGCT AGAGAGTTTG AGGATTGCTT TTTAAAAAAG ACAGCAAACT TTTTTTTTTA
TTTAAAAAAA GATATATTAA CAGTTTTAGA AGTCAGTAGA ATAAAATCTT AAAGCACTCA
TAATATGGCA TCCTTCAATT TCTGTATAAA AGCAGATCTT TTTAAAAAAG ATACTTCTGT
AACTTAAGAA ACCTGGCATT TAAATCATAT TTTGTCTTTA GGTAAAAGCT TTGGTTTGTG
TTCGTGTTTT GTTTGTTTCA CTTGTTTCCC TCCCAGCCCC AAACCTTTTG TTCTCTCCGT
GAAACTTACC TTTCCCTTTT TCTTTCTCTT TTTTTTTTTG TATATTATTG TTTACAATAA
ATATACATTG CATTAAAAAG AAA
```

Figure 8a(2)

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

```
Met Asn Leu Leu Asp Pro Phe Met Lys Met Thr Asp Glu Gln Glu Lys
 1               5                  10                  15
Gly Leu Ser Gly Ala Pro Ser Pro Thr Met Ser Glu Asp Ser Ala Gly
            20                  25                  30
Ser Pro Cys Pro Ser Gly Ser Gly Ser Asp Thr Glu Asn Thr Arg Pro
        35                  40                  45
Gln Glu Asn Thr Phe Pro Lys Gly Glu Pro Asp Leu Lys Lys Glu Ser
    50                  55                  60
Glu Glu Asp Lys Phe Pro Val Cys Ile Arg Glu Ala Val Ser Gln Val
65                  70                  75                  80
Leu Lys Gly Tyr Asp Trp Thr Leu Val Pro Met Pro Val Arg Val Asn
                85                  90                  95
Gly Ser Ser Lys Asn Lys Pro His Val Lys Arg Pro Met Asn Ala Phe
            100                 105                 110
Met Val Trp Ala Gln Ala Ala Arg Arg Lys Leu Ala Asp Gln Tyr Pro
        115                 120                 125
His Leu His Asn Ala Glu Leu Ser Lys Thr Leu Gly Lys Leu Trp Arg
    130                 135                 140
Leu Leu Asn Glu Ser Glu Lys Arg Pro Phe Val Glu Glu Ala Glu Arg
145                 150                 155                 160
Leu Arg Val Gln His Lys Lys Asp His Pro Asp Tyr Lys Tyr Gln Pro
                165                 170                 175
Arg Arg Arg Lys Ser Val Lys Asn Gly Gln Ala Glu Ala Glu Glu Ala
            180                 185                 190
Thr Glu Gln Thr His Ile Ser Pro Asn Ala Ile Phe Lys Ala Leu Gln
        195                 200                 205
Ala Asp Ser Pro His Ser Ser Ser Gly Met Ser Glu Val His Ser Pro
    210                 215                 220
Gly Glu His Ser Gly Gln Ser Gln Gly Pro Pro Thr Pro Pro Thr Thr
225                 230                 235                 240
Pro Lys Thr Asp Val Gln Pro Gly Lys Ala Asp Leu Lys Arg Glu Gly
                245                 250                 255
Arg Pro Leu Pro Glu Gly Gly Arg Gln Pro Pro Ile Asp Phe Arg Asp
            260                 265                 270
Val Asp Ile Gly Glu Leu Ser Ser Asp Val Ile Ser Asn Ile Glu Thr
        275                 280                 285
Phe Asp Val Asn Glu Phe Asp Gln Tyr Leu Pro Pro Asn Gly His Pro
    290                 295                 300
Gly Val Pro Ala Thr His Gly Gln Val Thr Tyr Thr Gly Ser Tyr Gly
305                 310                 315                 320
Ile Ser Ser Thr Ala Ala Thr Pro Ala Ser Ala Gly His Val Trp Met
                325                 330                 335
Ser Lys Gln Gln Ala Pro Pro Pro Pro Pro Gln Gln Pro Pro Gln Ala
            340                 345                 350
Pro Pro Ala Pro Gln Ala Pro Pro Gln Pro Gln Ala Ala Pro Pro Gln
        355                 360                 365
Gln Pro Ala Ala Pro Pro Gln Gln Pro Gln Ala His Thr Leu Thr Thr
    370                 375                 380
```

Figure 8a(3)

```
Leu Ser Ser Glu Pro Gly Gln Ser Gln Arg Thr His Ile Lys Thr Glu
385                 390                 395                 400
Gln Leu Ser Pro Ser His Tyr Ser Glu Gln Gln Gln His Ser Pro Gln
                    405                 410                 415
Gln Ile Ala Tyr Ser Pro Phe Asn Leu Pro His Tyr Ser Pro Ser Tyr
            420                 425                 430
Pro Pro Ile Thr Arg Ser Gln Tyr Asp Tyr Thr Asp His Gln Asn Ser
        435                 440                 445
Ser Ser Tyr Tyr Ser His Ala Ala Gly Gln Gly Thr Gly Leu Tyr Ser
    450                 455                 460
Thr Phe Thr Tyr Met Asn Pro Ala Gln Arg Pro Met Tyr Thr Pro Ile
465                 470                 475                 480
Ala Asp Thr Ser Gly Val Pro Ser Ile Pro Gln Thr His Ser Pro Gln
                    485                 490                 495
His Trp Glu Gln Pro Val Tyr Thr Gln Leu Thr Arg Pro
            500                 505
```


Figure 8a(4)

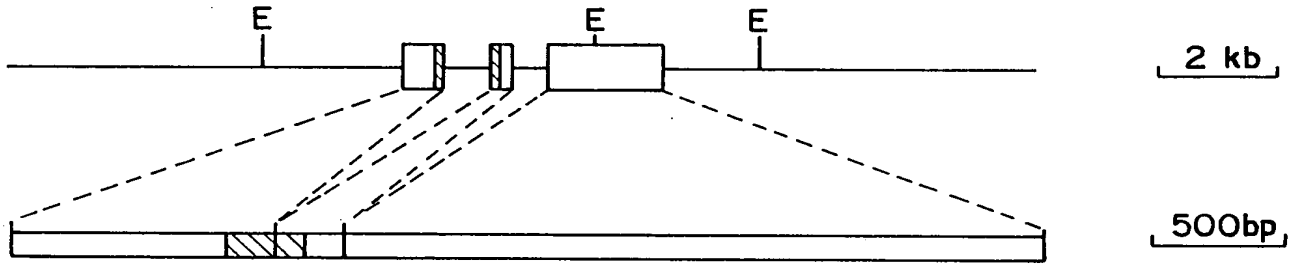

FIG.8b

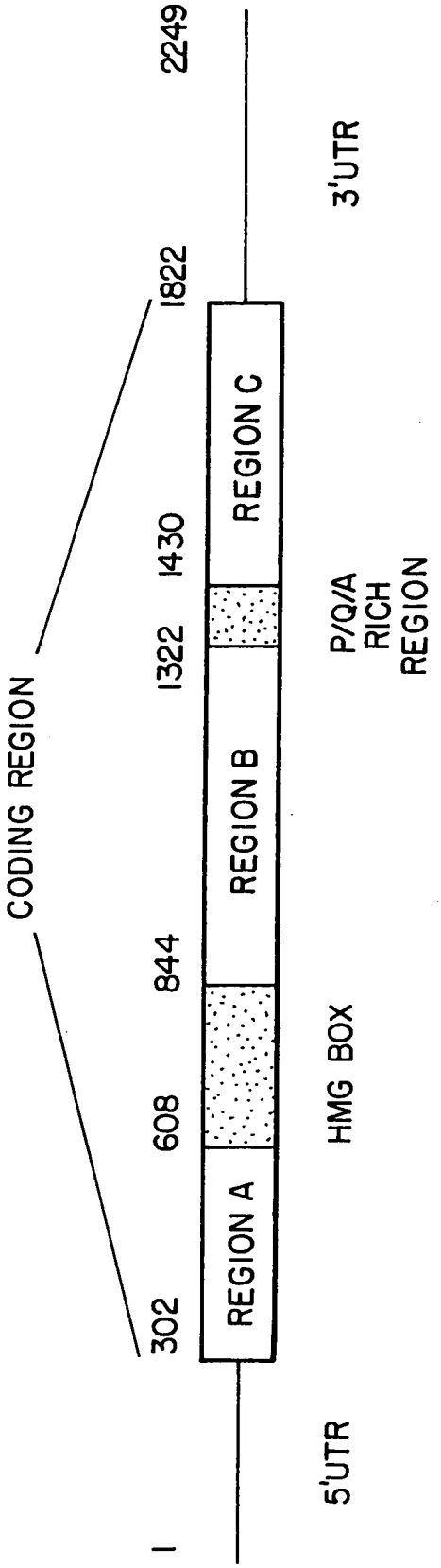

FIG.9

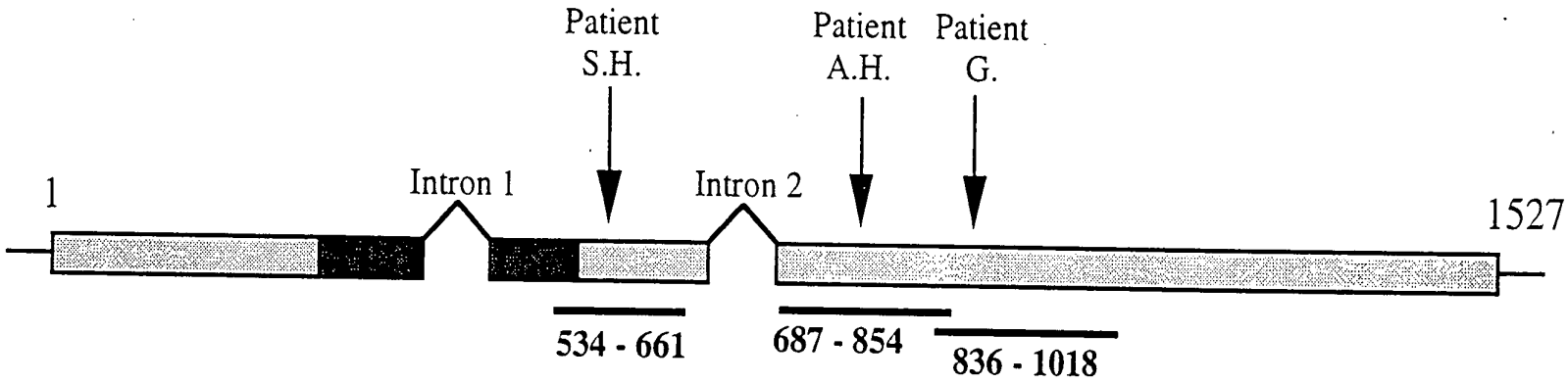

FIG.10a

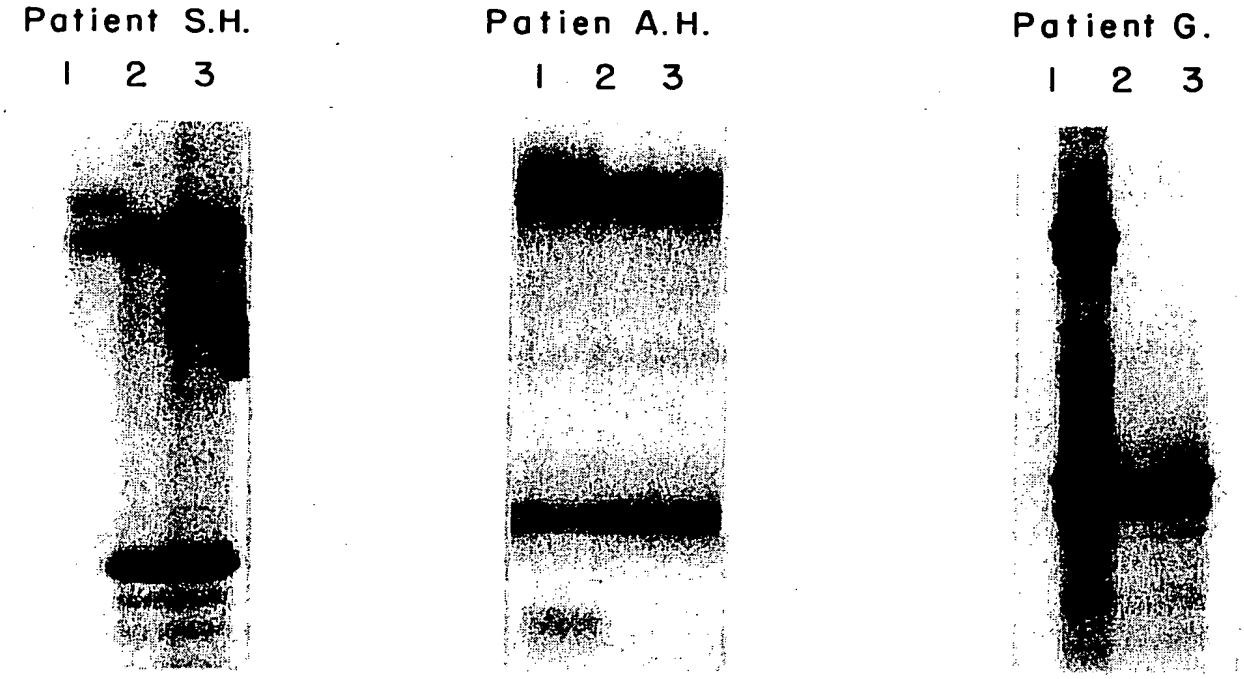

FIG.10b

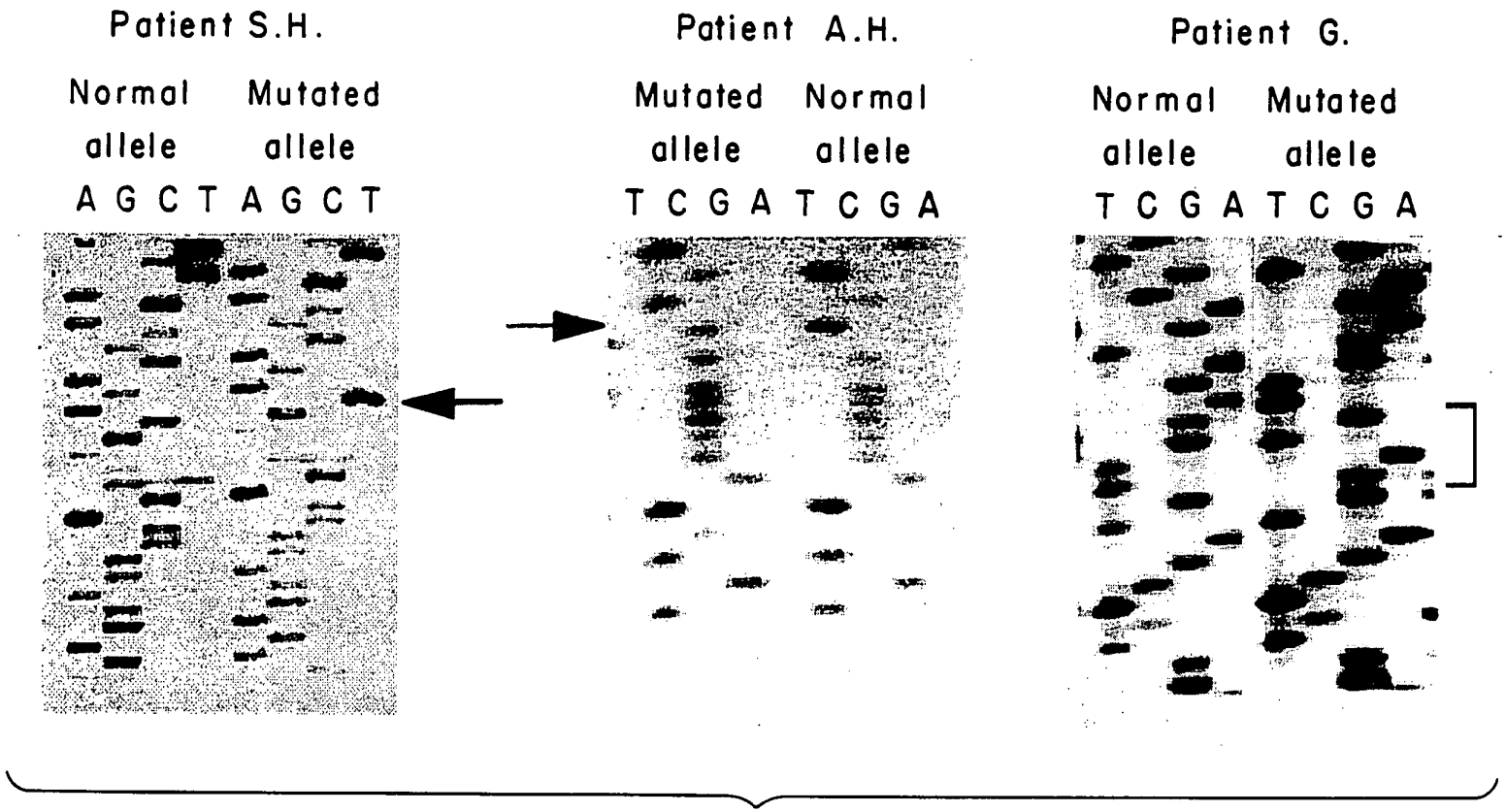

FIG.10c